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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/863,818A

DATE: 11/08/2001

TIME: 08:07:10

Input Set : A:\DX01170Kseq1stg.txt

Output Set: N:\CRF3\11082001\I863818A.raw

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p.5

3 <110> APPLICANT: Gorman, Daniel M.
 5 <120> TITLE OF INVENTION: MAMMALIAN RECEPTOR PROTEINS; RELATED REAGENTS AND METHODS
 7 <130> FILE REFERENCE: DX01170K
 9 <140> CURRENT APPLICATION NUMBER: 09/863,818A
 10 <141> CURRENT FILING DATE: 2001-05-23
 12 <150> PRIOR APPLICATION NUMBER: US 60/206,862
 13 <151> PRIOR FILING DATE: 2000-05-24
 15 <160> NUMBER OF SEQ ID NOS: 22
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1796
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
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 25 <221> NAME/KEY: CDS
 26 <222> LOCATION: (4)..(1509)
 27 <223> OTHER INFORMATION:
 30 <220> FEATURE:
 31 <221> NAME/KEY: mat_peptide
 32 <222> LOCATION: (46)..()
 33 <223> OTHER INFORMATION:
 36 <400> SEQUENCE: 1
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 39 -10 -5 -1 1
 41 gta ccc cga gag ccg acc gtt caa tgt ggc tct gaa act ggg cca tct 96
 42 Val Pro Arg Glu Pro Thr Val Gln Cys Gly Ser Glu Thr Gly Pro Ser
 43 5 10 15
 45 cca gag tgg atg cta caa cat gat cta atc ccg gga gac ttg agg gac 144
 46 Pro Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp
 47 20 25 30
 49 ctc cga gta gaa cct gtt aca act agt gtt gca aca ggg gac tat tca 192
 50 Leu Arg Val Glu Pro Val Thr Thr Ser Val Ala Thr Gly Asp Tyr Ser
 51 35 40 45
 53 att ttg atg aat gta agc tgg gta ctc cgg gca gat gcc agc atc cgc 240
 54 Ile Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg
 55 50 55 60 65
 57 ttg ttg aag gcc acc aag att tgt gtg acg ggc aaa agc aac ttc cag 288
 58 Leu Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln
 59 70 75 80
 61 tcc tac agc tgt gtg agg tgc aat tac aca gag gcc ttc cag act cag 336
 62 Ser Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln
 63 85 90 95
 65 acc aga ccc tct ggt ggt aaa tgg aca ttt tcc tat atc ggc ttc cct 384
 66 Thr Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro
 67 100 105 110
 69 gta gag ctg aac aca gtc tat ttc att ggg gcc cat aat att cct aat 432

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70	Val	Glu	Leu	Asn	Thr	Val	Tyr	Phe	Ile	Gly	Ala	His	Asn	Ile	Pro	Asn	
71		115					120					125					
73	gca	aat	atg	aat	gaa	gat	ggc	cct	tcc	atg	tct	gtg	aat	ttc	acc	tca	480
74	Ala	Asn	Met	Asn	Glu	Asp	Gly	Pro	Ser	Met	Ser	Val	Asn	Phe	Thr	Ser	
75	130					135					140				145		
77	cca	ggc	tgc	cta	gac	cac	ata	atg	aaa	tat	aaa	aaa	aag	tgt	gtc	aag	528
78	Pro	Gly	Cys	Leu	Asp	His	Ile	Met	Lys	Tyr	Lys	Lys	Lys	Cys	Val	Lys	
79					150					155					160		
81	gcc	gga	agc	ctg	tgg	gat	ccg	aac	atc	act	gct	tgt	aag	aag	aat	gag	576
82	Ala	Gly	Ser	Leu	Trp	Asp	Pro	Asn	Ile	Thr	Ala	Cys	Lys	Lys	Asn	Glu	
83				165					170					175			
85	gag	aca	gta	gaa	gtg	aac	ttc	aca	acc	act	ccc	ctg	gga	aac	aga	tac	624
86	Glu	Thr	Val	Glu	Val	Asn	Phe	Thr	Thr	Thr	Pro	Leu	Gly	Asn	Arg	Tyr	
87		180					185						190				
89	atg	gct	ctt	atc	caa	cac	agc	act	atc	atc	ggg	ttt	tct	cag	gtg	ttt	672
90	Met	Ala	Leu	Ile	Gln	His	Ser	Thr	Ile	Ile	Gly	Phe	Ser	Gln	Val	Phe	
91		195				200					205						
93	gag	cca	cac	cag	aag	aaa	caa	acg	cga	gct	tca	gtg	gtg	att	cca	gtg	720
94	Glu	Pro	His	Gln	Lys	Lys	Gln	Thr	Arg	Ala	Ser	Val	Val	Ile	Pro	Val	
95	210				215					220					225		
97	act	ggg	gat	agt	gaa	ggt	gct	acg	gtg	cag	ctg	act	cca	tat	ttt	cct	768
98	Thr	Gly	Asp	Ser	Glu	Gly	Ala	Thr	Val	Gln	Leu	Thr	Pro	Tyr	Phe	Pro	
99				230					235					240			
101	act	tgt	ggc	agc	gac	tgc	atc	cga	cat	aaa	gga	aca	gtt	gtg	ctc	tgc	816
102	Thr	Cys	Gly	Ser	Asp	Cys	Ile	Arg	His	Lys	Gly	Thr	Val	Val	Leu	Cys	
103				245					250					255			
105	cca	caa	aca	ggc	gtc	cct	ttc	cct	ctg	gat	aac	aac	aaa	agc	aag	ccg	864
106	Pro	Gln	Thr	Gly	Val	Pro	Phe	Pro	Leu	Asp	Asn	Asn	Lys	Ser	Lys	Pro	
107		260					265						270				
109	gga	ggc	tgg	ctg	cct	ctc	ctc	ctg	ctg	tct	ctg	ctg	gtg	gcc	aca	tgg	912
110	Gly	Gly	Trp	Leu	Pro	Leu	Leu	Leu	Leu	Ser	Leu	Leu	Val	Ala	Thr	Trp	
111		275				280					285						
113	gtg	ctg	gtg	gca	ggg	atc	tat	cta	atg	tgg	agg	cac	gaa	agg	atc	aag	960
114	Val	Leu	Val	Ala	Gly	Ile	Tyr	Leu	Met	Trp	Arg	His	Glu	Arg	Ile	Lys	
115	290				295					300					305		
117	aag	act	tcc	ttt	tct	acc	acc	aca	cta	ctg	ccc	ccc	att	aag	gtt	ctt	1008
118	Lys	Thr	Ser	Phe	Ser	Thr	Thr	Thr	Leu	Leu	Pro	Pro	Ile	Lys	Val	Leu	
119				310					315					320			
121	gtg	gtt	tac	cca	tct	gaa	ata	tgt	ttc	cat	cac	aca	att	tgt	tac	ttc	1056
122	Val	Val	Tyr	Pro	Ser	Glu	Ile	Cys	Phe	His	His	Thr	Ile	Cys	Tyr	Phe	
123				325					330					335			
125	act	gaa	ttt	ctt	caa	aac	cat	tgc	aga	agt	gag	gtc	atc	ctt	gaa	aag	1104
126	Thr	Glu	Phe	Leu	Gln	Asn	His	Cys	Arg	Ser	Glu	Val	Ile	Leu	Glu	Lys	
127		340					345					350					
129	tgg	cag	aaa	aag	aaa	ata	gca	gag	atg	ggt	cca	gtg	cag	tgg	ctt	gcc	1152
130	Trp	Gln	Lys	Lys	Lys	Ile	Ala	Glu	Met	Gly	Pro	Val	Gln	Trp	Leu	Ala	
131		355				360					365						
133	act	caa	aag	aag	gca	gca	gac	aaa	gtc	gtc	ttc	ctt	ctt	tcc	aat	gac	1200
134	Thr	Gln	Lys	Lys	Ala	Ala	Asp	Lys	Val	Val	Phe	Leu	Leu	Ser	Asn	Asp	

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135 370          375          380          385
137 gtc aac agt gtg tgc gat ggt acc tgt ggc aag agc gag ggc agt ccc      1248
138 Val Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro
139          390          395          400
141 agt gag aac tct caa gac ctc ttc ccc ctt gcc ttt aac ctt ttc tgc      1296
142 Ser Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys
143          405          410          415
145 agt gat cta aga agc cag att cat ctg cac aaa tac gtg gtg gtc tac      1344
146 Ser Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr
147          420          425          430
149 ttt aga gag att gat aca aaa gac gat tac aat gct ctc agt gtc tgc      1392
150 Phe Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys
151          435          440          445
153 ccc aag tac cac ctc atg aag gat gcc act gct ttc tgt gca gaa ctt      1440
154 Pro Lys Tyr His Leu Met Lys Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu
155 450          455          460          465
157 ctc cat gtc aag cag cag gtg tca gca gga aaa aga tca caa gcc tgc      1488
158 Leu His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys
159          470          475          480
161 cac gat ggc tgc tgc tcc ttg tagccaccc atgagaagca agagacctta      1539
162 His Asp Gly Cys Cys Ser Leu
163          485
165 aaggttctct atcccaccaa ttacagggaa aaaacgtgtg atgacctga agcttactat      1599
167 gcagcctaca aacagcctta gtaattaaaa cattttatac caataaaatt ttcaaataatt      1659
169 gctaactaat gtagcattaa ctaacgattg gaaactacat ttacaacttc aaagctgttt      1719
171 tatacataga aatcaattac agctttaatt gaaaactgta accattttga taatgcaaca      1779
173 ataaagcatc ttcagcc      1796
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177 <211> LENGTH: 502
178 <212> TYPE: PRT
179 <213> ORGANISM: Homo sapiens
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188          5          10          15
191 Glu Trp Met Leu Gln His Asp Leu Ile Pro Gly Asp Leu Arg Asp Leu
192          20          25          30
195 Arg Val Glu Pro Val Thr Ser Val Ala Thr Gly Asp Tyr Ser Ile
196 35          40          45          50
199 Leu Met Asn Val Ser Trp Val Leu Arg Ala Asp Ala Ser Ile Arg Leu
200          55          60          65
203 Leu Lys Ala Thr Lys Ile Cys Val Thr Gly Lys Ser Asn Phe Gln Ser
204          70          75          80
207 Tyr Ser Cys Val Arg Cys Asn Tyr Thr Glu Ala Phe Gln Thr Gln Thr
208          85          90          95
211 Arg Pro Ser Gly Gly Lys Trp Thr Phe Ser Tyr Ile Gly Phe Pro Val
212          100          105          110
215 Glu Leu Asn Thr Val Tyr Phe Ile Gly Ala His Asn Ile Pro Asn Ala

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216 115          120          125          130
219 Asn Met Asn Glu Asp Gly Pro Ser Met Ser Val Asn Phe Thr Ser Pro
220          135          140          145
223 Gly Cys Leu Asp His Ile Met Lys Tyr Lys Lys Lys Cys Val Lys Ala
224          150          155          160
227 Gly Ser Leu Trp Asp Pro Asn Ile Thr Ala Cys Lys Lys Asn Glu Glu
228          165          170          175
231 Thr Val Glu Val Asn Phe Thr Thr Thr Pro Leu Gly Asn Arg Tyr Met
232          180          185          190
235 Ala Leu Ile Gln His Ser Thr Ile Ile Gly Phe Ser Gln Val Phe Glu
236 195          200          205          210
239 Pro His Gln Lys Lys Gln Thr Arg Ala Ser Val Val Ile Pro Val Thr
240          215          220          225
243 Gly Asp Ser Glu Gly Ala Thr Val Gln Leu Thr Pro Tyr Phe Pro Thr
244          230          235          240
247 Cys Gly Ser Asp Cys Ile Arg His Lys Gly Thr Val Val Leu Cys Pro
248          245          250          255
251 Gln Thr Gly Val Pro Phe Pro Leu Asp Asn Asn Lys Ser Lys Pro Gly
252          260          265          270
255 Gly Trp Leu Pro Leu Leu Leu Leu Ser Leu Leu Val Ala Thr Trp Val
256 275          280          285          290
259 Leu Val Ala Gly Ile Tyr Leu Met Trp Arg His Glu Arg Ile Lys Lys
260          295          300          305
263 Thr Ser Phe Ser Thr Thr Thr Leu Leu Pro Pro Ile Lys Val Leu Val
264          310          315          320
267 Val Tyr Pro Ser Glu Ile Cys Phe His His Thr Ile Cys Tyr Phe Thr
268          325          330          335
271 Glu Phe Leu Gln Asn His Cys Arg Ser Glu Val Ile Leu Glu Lys Trp
272          340          345          350
275 Gln Lys Lys Lys Ile Ala Glu Met Gly Pro Val Gln Trp Leu Ala Thr
276 355          360          365          370
279 Gln Lys Lys Ala Ala Asp Lys Val Val Phe Leu Leu Ser Asn Asp Val
280          375          380          385
283 Asn Ser Val Cys Asp Gly Thr Cys Gly Lys Ser Glu Gly Ser Pro Ser
284          390          395          400
287 Glu Asn Ser Gln Asp Leu Phe Pro Leu Ala Phe Asn Leu Phe Cys Ser
288          405          410          415
291 Asp Leu Arg Ser Gln Ile His Leu His Lys Tyr Val Val Val Tyr Phe
292          420          425          430
295 Arg Glu Ile Asp Thr Lys Asp Asp Tyr Asn Ala Leu Ser Val Cys Pro
296 435          440          445          450
299 Lys Tyr His Leu Met Lys Asp Ala Thr Ala Phe Cys Ala Glu Leu Leu
300          455          460          465
303 His Val Lys Gln Gln Val Ser Ala Gly Lys Arg Ser Gln Ala Cys His
304          470          475          480
307 Asp Gly Cys Cys Ser Leu
308          485
311 <210> SEQ ID NO: 3
312 <211> LENGTH: 637

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Input Set : A:\DX01170Kseqlstg.txt

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313 <212> TYPE: DNA
314 <213> ORGANISM: Mus musculus
316 <220> FEATURE:
317 <221> NAME/KEY: CDS
318 <222> LOCATION: (1)..(210)
319 <223> OTHER INFORMATION:
322 <400> SEQUENCE: 3
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325 1          5          10          15
327 ggg gga gca gac ctc aaa ggc gac tat aat gcc ctg agt gtc tgc ccc      96
328 Gly Gly Ala Asp Leu Lys Gly Asp Tyr Asn Ala Leu Ser Val Cys Pro
329          20          25          30
331 caa tat cat ctc atg aag gac gcc aca gct ttc cac aca gaa ctt ctc      144
332 Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu
333          35          40          45
335 aag gct acg cag agc atg tca gtg aag aaa cgc tca caagcc tgc cat      192
336 Lys Ala Thr Gln Ser Met Ser Val Lys Lys Arg Ser Gln Ala Cys His
337          50          55          60
339 gat agc tgt tca ccc ttg tagtccaccc gggggaatag agactctgaa      240
340 Asp Ser Cys Ser Pro Leu
341 65          70
343 gccttccctac tctcccttcc agtgacaaat gctgtgtgac gactctgaaa tgtgtgggag      300
345 aggctgtgtg gaggtagtgc tatgtacaaa cttgctttaa aactggagtt tgcaaagtca      360
347 acctgagcat acacgctga ggctagtcat tggtctggatt tatgaagaca acacagttac      420
349 agacaataat gagtgggacc tacatttggg atatacccaa agctgggtaa tgattatcac      480
351 tgagaaccac gcactctggc catgaggtaa tacggcactt ccctgtcagg ctgtctgtca      540
353 gggttgggtct gtcttgcact gcccatgctc tatgtctgcac gtagaccgtt ttgtaacatt      600
355 ttaatctgtt aatgaataat ccgtttggga ggctctc      637
358 <210> SEQ ID NO: 4
359 <211> LENGTH: 70
360 <212> TYPE: PRT
361 <213> ORGANISM: Mus musculus
363 <400> SEQUENCE: 4
365 Asp Phe Ser Ser Gln Thr His Leu His Lys Tyr Leu Glu Val Tyr Leu
366 1          5          10          15
369 Gly Gly Ala Asp Leu Lys Gly Asp Tyr Asn Ala Leu Ser Val Cys Pro
370          20          25          30
373 Gln Tyr His Leu Met Lys Asp Ala Thr Ala Phe His Thr Glu Leu Leu
374          35          40          45
377 Lys Ala Thr Gln Ser Met Ser Val Lys Lys Arg Ser Gln Ala Cys His
378          50          55          60
381 Asp Ser Cys Ser Pro Leu
382 65          70
385 <210> SEQ ID NO: 5
386 <211> LENGTH: 2308
387 <212> TYPE: DNA
388 <213> ORGANISM: Homo sapiens
390 <220> FEATURE:

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VERIFICATION SUMMARY

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L:589 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:590 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:790 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:1244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1250 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1275 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1278 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1279 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1282 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1283 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1526 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1546 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1550 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:1554 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10